

Jongmin Kim

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Education

- Ph.D. California Institute of Technology, Biology** - Pasadena, CA, USA June 2007
Advisor: Prof. Erik Winfree
Thesis: “*In vitro* synthetic transcriptional networks”
- B.S., Pohang University of Science and Technology, Life Science** - Pohang, Korea August 2000
Graduated *summa cum laude*
Thesis Advisor: Prof. Byung-Ha Oh
Thesis: “Purification and Characterization of Caspase”

Experience

- Assistant Professor, Life Sciences, POSTECH** – Pohang, Gyeongbuk, Korea May 2018–Present
Synthetic Biology and Molecular Computing
- Senior Scientist, NuProbe USA Inc.** – Cambridge, MA, USA March 2018–April 2018
DNA toehold probes for cell-free DNA detection
- Postdoctoral Research Fellow, Harvard University** – Boston, MA, USA March 2014–April 2018
Wyss Institute for Biologically Inspired Engineering, Advisor: Prof. Peng Yin
- Postdoctoral Scholar, California Institute of Technology** – Pasadena, CA, USA March 2010–March 2014
Department of Bioengineering, Advisor: Prof. Richard Murray
- Senior Researcher, CbsBioscience Inc.** – Daejeon, Korea Jan 2007–March 2010
Prognostic markers of hepatocellular carcinoma

Selected Publications

- **Kim J***, Zhou Y*, Carlson PD, Teichmann M, Chaudhary S, Simmel FC, Silver PA, Collins JJ, Yin P, Green AA, De novo-designed translation-repressing riboregulators for multi-input cellular logic, *Nature Chemical Biology* 15:1173–1182, 2019. *, co-first authors. – **Cover article**
- Green LN, Subramanian HKK, Mardanlou V, **Kim J**, Hariadi R, Franco E, Autonomous dynamic control of DNA nanostructure self-assembly, *Nature Chemistry* 11:510–520, 2019. – **News & Views** by Tim Liedl in *Nature Chemistry* 11:497–499.
- Green AA*, **Kim J***, Ma D, Silver PA, Collins JJ, Yin P, Complex cellular logic computation using ribocomputing devices, *Nature* 548:117–121, 2017. *, co-first authors.
- Weitz M, **Kim J**, Kapsner K, Winfree E, Franco E, Simmel FC, Diversity in the dynamical behaviour of a compartmentalized programmable biochemical oscillator, *Nature Chemistry* 6:295–302, 2014. – **Cover article**
- **Kim J**, Khetarpal I, Sen S, Murray RM, Synthetic circuit for exact adaptation and fold-change detection, *Nucleic Acids Research* 42:6078–6089, 2014.
- **Kim J**, Winfree E, Synthetic *in vitro* transcriptional oscillators, *Molecular Systems Biology* 7:465, 2011.
- Kwon JH*, **Kim J***, Park JY, Hong SM, Park CW, Hong SJ, Park SY, Choi YJ, Do IG, Joh JW, Kim DS, Choi KY, 2010, Overexpression of HMGB2 is associated with tumor aggressiveness and prognosis of hepatocellular carcinoma, *Clinical Cancer Research* 16:5511–21 (*, co-first authors). – **Highlights in Clinical Cancer Research**
- **Kim J**, White KS, Winfree E, Construction of an *in vitro* bistable circuit from synthetic transcriptional switches, *Molecular Systems Biology* 2:68, 2006. – **News & Views** by Michael Simpson in *Molecular Systems Biology* 2:69.

Patents

- Compositions comprising riboregulators and methods of use thereof (PCT pending)
- Markers for prognosis of liver cancer (Korean patent 10-0964193, PCT applied for)
- Protein markers for diagnosis of liver cancer progression (Korean patent 10-1004960)
- Protein markers for early diagnosis of liver cancer (Korean patent pending, PCT applied for)
- Compositions, kits, and methods for predicting prognosis of liver cancer (Korean patent pending, PCT applied for)
- Markers for prognosis of liver cancer (Korean patent pending)

Honors & Awards

- Wyss Institute cross-platform fellowship 2014–2017
Korea Foundation for Advanced Studies predoctoral fellowship 2000–2005
Korea Foundation for Advanced Studies undergraduate fellowship 1998–2000
Pohang University of Science and Technology full-tuition scholarship - ranked first in entrance exam 1997–2000

Professional Service & Activities

- Reviewer for Nature Chemistry, Chemical Science, ACS Synthetic Biology, Nucleic Acids Research, IEEE Transactions on Biomedical Circuits and Systems, New Generation Computing, IEEE Conference on Decision and Control, IEEE American Control Conference, IEEE European Control Conference, International Conference on DNA Computing and Molecular Programming
- Organizer for an all-day wet lab tutorial “Genelets: synthetic *in vitro* transcriptional circuits” with Josh Bishop and Elisa Franco for 17th international conference on DNA computing and molecular programming in 2011
- Instructor for cell-free extract preparation with Anu Thubagere as part of “Cell-free TX-TL systems for synthetic biology” workshop at California Institute of Technology in 2013

Selected Presentations

- Complex cellular logic computation using ribocomputing devices, Gordon Research Seminar - Synthetic Biology, 2017.
- Complex cellular logic computation using ribocomputing devices, The First CompuGene Symposium, 2017.
- Complex cellular logic computation using ribocomputing devices, The 14th Annual Conference on Foundations of Nanoscience, 2017.
- Complex cellular logic computation using ribocomputing devices, Engineering Biology Research Consortium retreat, 2017.
- Ribocomputing devices for sophisticated *in vivo* logic computation, The 3rd ACM International Conference on Nanoscale Computing and Communication, 2016.
- Ribocomputing devices for sophisticated *in vivo* logic computation, The 22nd International Conference on DNA Computing and Molecular Programming, 2016.
- RNA information processors for complex *in vivo* logic computation, The 7th Molecular Programming Project workshop, 2016.
- Ribocomputers for *in vivo* logic computation, Pohang University of Science and Technology, 2015.
- Global dynamical structure reconstruction from subnetwork dynamical structure reconstruction: Applications to biochemical reaction networks, IEEE Conference on Decision and Control, 2015.
- *In vivo* application of an inhibitory RNA aptamer against T7 RNA polymerase, The 2nd annual winter q-bio meeting, 2014.
- Synthetic circuit for exact adaptation and fold-change detection, The 19th International Conference on DNA Computing and Molecular Programming, 2013.
- Synthetic biology: Bottom-up approaches and applications, Yonsei University, 2013.
- Synthetic biology: Bottom-up approaches and applications, Seoul National University, 2013.
- Programmability of synthetic transcriptional networks, The 4th Molecular Programming Project workshop, 2012.
- Neural network computation with DNA circuits, International Brain Research Symposium, 2012.
- Synthetic biology: Bottom-up approaches and applications, Pohang University of Science and Technology, 2012.
- Analysis and design of a synthetic transcriptional network for exact adaptation, IEEE Biomedical Circuits and Systems Conference, 2011.
- Workshop: “Genelets: synthetic *in vitro* transcriptional circuits”, The 17th international conference on DNA computing and molecular programming, 2011.
- Molecular classification and prediction of survival in hepatocellular carcinoma patients by gene expression profiling, Pohang University of Science and Technology, 2011.
- *In vitro* synthetic oscillators, Non-coding RNAs & Synthetic Biology, 2009.
- *In vitro* synthetic oscillators, Synthetic biology 4.0, 2008.
- *In vitro* synthetic oscillators, BiosysBio, 2008. - **Best synthetic biology presentation award**

Full List of Publications

Journals

1. Heo T[†], Kang H[†], Choi S[†], **Kim J***, Detection of pks island mRNAs using toehold sensors in *Escherichia coli*, *Life* 11:1280, 2021. [†], co-first authors.
2. Yeung E, **Kim J**, Yuan Y, Gonçalves J, Murray RM, Data-driven network models for genetic circuits from time-series data with incomplete measurements, *Journal of the Royal Society Interface* 18:20210413, 2021.
3. Hong S[†], Jeong D[†], Ryan J[†], Foo M*, Tang X*, **Kim J***, Design and evaluation of synthetic RNA-based incoherent feed-forward loop circuits, *Biomolecules* 11:1182, 2021. [†], co-first authors. *, co-corresponding authors.
4. Pieters PA, Nathalia BL, van der Linden AJ, Yin P, **Kim J***, Huck WTS*, de Greef TFA*, Cell-free characterization of coherent feed-forward loop-based synthetic genetic circuits, *ACS Synthetic Biology* 10:1406–1416, 2021. *, co-corresponding authors.
5. Hong S[†], Kim J[†], **Kim J**, Multilevel gene regulation using switchable transcription terminator and toehold switch in *Escherichia coli*, *Applied Sciences* 11:4532, 2021. [†], co-first authors.
6. **Kim J***, Quijano JF, Kim J, Yeung E, Murray RM, Synthetic logic circuits using RNA aptamer against T7 RNA polymerase, *Biotechnology Journal*, 2021.

7. Hwang Y, Kim SG, Jang S, **Kim J***, Jung GY*, Signal amplification and optimization of riboswitch-based hybrid inputs by modular and titratable toehold switches, *Journal of Biological Engineering* 15:11, 2021. *, co-corresponding authors.
8. Paulino NMG, Foo M, **Kim J**, Bates DG, On the stability of nucleic acid feedback control systems, *Automatica* 119:109103, 2020.
9. **Kim J**, Franco E, RNA nanotechnology in synthetic biology, *Current Opinion in Biotechnology* 63:135–141, 2020.
10. **Kim J***, Zhou Y*, Carlson PD, Teichmann M, Chaudhary S, Simmel FC, Silver PA, Collins JJ, Yin P, Green AA, De novo-designed translation-repressing riboregulators for multi-input cellular logic, *Nature Chemical Biology* 15:1173–1182, 2019. *, co-first authors. – **Cover article**
11. Jin M, Garreau N, Kim Y, **Kim J***, Yin P*, Programmable CRISPR-Cas repression, activation, and computation with sequence-independent targets and triggers, *ACS Synthetic Biology* 8:1583–1589, 2019. *, co-corresponding authors.
12. Paulino NMG, Foo M, **Kim J**, Bates DG, PID and state feedback controllers using DNA strand displacement reactions, *IEEE Control Systems Letters* 3:805–810, 2019.
13. Paulino NMG, Foo M, **Kim J**, Bates DG, Robustness analysis of a nucleic acid controller for a dynamic biomolecular process using the structured singular value, *Journal of Process Control* 78:34–44, 2019.
14. Jeong D*, Klocke M*, Agarwal S, Kim J, Choi S, Franco E, **Kim J**, Cell-Free Synthetic Biology Platform for Engineering Synthetic Biological Circuits and Systems, *Methods and Protocols* 2:39, 2019. *, co-first authors.
15. Green LN, Subramanian HKK, Mardanlou V, **Kim J**, Hariadi R, Franco E, Autonomous dynamic control of DNA nanostructure self-assembly, *Nature Chemistry* 11:510–520, 2019. – **News & Views** by Tim Liedl in *Nature Chemistry* 11:497–499.
16. **Kim J**, Green AA, Yin P, Ribocomputing: Cellular logic computation using RNA devices, *Biochemistry* 57:883–885, 2018.
17. Mardanlou V, Yaghoubi KC, Green LN, Subramanian HK, Hariadi RF, **Kim J**, Franco E, A coarse-grained model captures the temporal evolution of DNA nanotube length distributions, *Natural Computing* 17:183–199, 2018.
18. Green AA*, **Kim J***, Ma D, Silver PA, Collins JJ, Yin P, Complex cellular logic computation using ribocomputing devices, *Nature* 548:117–121, 2017. *, co-first authors.
19. Foo M, Kim J, **Kim J**, Bates DG, Proportional-integral degradation (PI-Deg) control allows accurate tracking of biomolecular concentrations with fewer chemical reactions, *IEEE Life Sciences Letters* 2:55–58, 2016.
20. Cuba C, Giordano G, **Kim J**, Blanchini F, Franco E, Molecular titration promotes oscillations and bistability in minimal network models with monomeric regulators, *ACS Synthetic Biology* 5:321–333, 2016.
21. Takahashi M, Chappell J, Hayes C, Sun ZZ, **Kim J**, Singhal V, Spring K, Al-Khabouri S, Fall C, Noireaux V, Murray RM, Lucks J, Rapidly characterizing the fast dynamics of RNA genetic circuitry with cell-free transcription-translation (TX-TL) systems, *ACS Synthetic Biology* 4:503–515, 2015.
22. Yordanov B, **Kim J**, Petersen R, Shudy A, Kulkarni VV, Phillips A, Computational design of nucleic acid feedback control circuits, *ACS Synthetic Biology* 3:600–616, 2014.
23. **Kim J**, Khetarpal I, Sen S, Murray RM, Synthetic circuit for exact adaptation and fold-change detection, *Nucleic Acids Research* 42:6078–6089, 2014.
24. Siegal-Gaskins D*, Tuza ZA*, **Kim J***, Noireaux V, Murray RM, Resource usage and gene circuit performance characterization in a cell-free 'breadboard', *ACS Synthetic Biology* 3:416–425, 2014. *, co-first authors.
25. Kulkarni VV, Kharisov E, Hovakimyan N, **Kim J**, Load capacity improvements in nucleic acid based systems using partially open feedback control, *ACS Synthetic Biology* 3:617–626, 2014.
26. Weitz M, **Kim J**, Kapsner K, Winfree E, Franco E, Simmel FC, Diversity in the dynamical behaviour of a compartmentalized programmable biochemical oscillator, *Nature Chemistry* 6:295–302, 2014. – **Cover article**
27. Subsoontorn P*, **Kim J***, Winfree E, Ensemble Bayesian analysis of bistability in a synthetic transcriptional switch, *ACS Synthetic Biology* 1:299–316, 2012. *, co-first authors.
28. Lee D, Do IG, Choi K, Sung CO, Jang KT, Choi D, Heo JS, Choi SH, **Kim J**, Park JY, Cha HJ, Joh JW, Choi KY, Kim DS, The expression of phospho-AKT1 and phospho-mTOR is associated with a favorable prognosis independent of PTEN expression in intrahepatic cholangiocarcinomas, *Modern Pathology* 25:131–139, 2012.
29. Cha HJ, **Kim J**, Hong SJ, Hong SM, Park JH, Kim ES, Choi YJ, Do IG, Joh JW, Kim DS, Choi KY, Overexpression of renal tumor antigen is associated with tumor invasion and poor prognosis of hepatocellular carcinoma, *Annals of Surgical Oncology Suppl* 3:S404–11, 2012.
30. Franco E, Friedrichs E, **Kim J**, Jungmann R, Murray RM, Winfree E, Simmel FC, Timing molecular motion and production with a synthetic transcriptional clock, *Proceedings of the National Academy of Sciences USA* 108:E784–E793, 2011. – **Highlights in Biopolymers**
31. **Kim J**, Winfree E, Synthetic *in vitro* transcriptional oscillators, *Molecular Systems Biology* 7:465, 2011.
32. Kwon JH*, **Kim J***, Park JY, Hong SM, Park CW, Hong SJ, Park SY, Choi YJ, Do IG, Joh JW, Kim DS, Choi KY, Overexpression of HMGB2 is associated with tumor aggressiveness and prognosis of hepatocellular carcinoma, *Clinical Cancer Research* 16:5511–21, 2010. *, co-first authors. – **Highlights in Clinical Cancer Research**

33. **Kim J**, Hong SJ, Park JY, Park JH, Yu YS, Park SY, Lim EK, Choi KY, Lee EK, Paik SS, Lee KG, Wang HJ, Do IG, Joh JW, Kim DS, Epithelial-mesenchymal transition gene signature to predict clinical outcome of hepatocellular carcinoma, *Cancer Science* 101:1521–28, 2010. – **A prognostic test (OncoHepa^{Test}) based on this study is licensed as new health technology by Ministry of Health and Welfare in Korea (Ministry of Health and Welfare Notice 2010-83)**
34. **Kim J***, Kim JM*, Hong SJ, Park JH, Park SY, Hwang T, Yi GS, Kim SH, Cho EY, Joh JW, Park JY, Kim DS, Increased expression of autophagy protein Beclin1 and LC3 in high-grade hepatocellular carcinoma and metastatic carcinoma, *Biochip Journal* 3:316–25, 2009. *, co-first authors.
35. Hong SJ*, **Kim J***, Park JH, Lim EK, Kim J, Choi YJ, Gu H, Kim SW, Choi KY, Joh JW, Kim DS, Proteomic profiling of human hepatocellular carcinoma tissues by two-dimensional electrophoresis and mass spectrometry, *Biochip Journal* 3:237–48, 2009. *, co-first authors.
36. **Kim J**, Hong SJ, Park JH, Lee CB, Kim SW, Gu H, Choi GS, Kwon CHD, Joh JW, Kim DS, Real-time reverse transcription PCR analysis for validation of transketolase gene in hepatocellular carcinoma tissues, *Biochip Journal* 3:130–8, 2009.
37. **Kim J**, Hong SJ, Park JH, Park SY, Kim SW, Cho EY, Do IG, Joh JW, Kim DS, Expression of cystathionine beta-synthase is downregulated in hepatocellular carcinoma and associated with poor prognosis, *Oncology Reports* 21:1449–54, 2009.
38. **Kim J**, Hong SJ, Lim EK, Yu YS, Kim SW, Roh JH, Do IG, Joh JW, Kim DS, Expression of nicotinamide N-methyltransferase in hepatocellular carcinoma is associated with poor prognosis, *Journal of Experimental and Clinical Cancer Research* 28:20, 2009.
39. **Kim J**, White KS, Winfree E, Construction of an *in vitro* bistable circuit from synthetic transcriptional switches, *Molecular Systems Biology* 2:68, 2006. – **News & Views** by Michael Simpson in *Molecular Systems Biology* 2:69.

Conference Papers & Book Chapters

1. Samaniego CC, **Kim J**, Franco E, Sequestration and delays enable the synthesis of a molecular derivative operator, *IEEE Conference on Decision and Control*, p. 5106-5112, 2020.
2. Paulino NMG, Foo M, de Greef TFA, **Kim J**, Bates DG, Minimally complex nucleic acid feedback control systems for first experimental implementations, *International Federation of Automatic Control*, p. 16745-16752, 2020.
3. Paulino NMG, Foo M, **Kim J**, Bates DG, PID and state feedback controllers using DNA strand displacement reactions, *IEEE Conference on Decision and Control*, p., 2019.
4. Paulino NMG, Foo M, **Kim J**, Bates DG, Uncertainty modelling and stability robustness analysis of nucleic acid-based feedback control systems, *IEEE Conference on Decision and Control*, p. 1077-1082, 2018.
5. Jafarnejadsani H, **Kim J**, Kulkarni VV, Hovakimyan N, Load capacity improvements in nucleic acid based systems using discrete-time feedback control, *The 5th International Conference on Control, Decision and Information Technology (CoDIT)*, p. 1–6, 2018.
6. Green AA, **Kim J**, Ma D, Silver PA, Collins JJ, Yin P, Ribocomputing devices for sophisticated *in vivo* logic computation, *The 3rd ACM International Conference on Nanoscale Computing and Communication*, p. 11, 2016.
7. Mardanlou V, Green LN, Subramanian HK, Hariadi RF, **Kim J**, Franco E, A coarse-grained model of DNA nanotube population growth, *The 22nd International Conference on DNA Computing and Molecular Programming*, p. 135–147, 2016.
8. Jafarnejadsani H, **Kim J**, Hovakimyan N, Kulkarni VV, Load capacity improvements in transcriptional systems using discrete-time L1-adaptive control, *Proceedings on 8th International Workshop on Bio-Design Automation*, p. 75–76, 2016.
9. Foo M, Sawlekar R, **Kim J**, Bates DG, Stan G-B, Kulkarni V, Biomolecular implementation of nonlinear system theoretic operators, *IEEE European Control Conference*, p. 1824–1831, 2016.
10. Schwarz-Schilling M, **Kim J**, Cuba C, Weitz M, Franco E, Simmel FC, Building a synthetic transcriptional oscillator, *Methods in Molecular Biology* 1342:185-199, 2016.
11. Yeung E, **Kim J**, Gonçalves J, Murray RM, Global network identification from reconstructed dynamical structure subnetworks: Applications to biochemical reaction networks, *IEEE Conference on Decision and Control*, p. 881–888, 2015.
12. Tuza ZA, Siegal-Gaskins D, **Kim J**, Szederkényi G, Analysis-based parameter estimation of an *in vitro* transcription-translation system, *IEEE European Control Conference*, p. 1560–1566, 2015.
13. Sun ZZ, **Kim J**, Singhal V, Murray RM, Protein degradation in a TX-TL cell-free expression system using ClpXP protease, *Technical Report*, 2015.
14. Yeung E, Ng A, **Kim J**, Sun ZZ, Murray RM, Modeling the effects of compositional context on promoter activity in an *E. coli* extract based transcription-translation system, *IEEE Conference on Decision and Control*, p. 5405–5412, 2014.
15. Sen S, **Kim J**, Murray RM, Designing robustness to temperature in a feedforward loop circuit, *IEEE Conference on Decision and Control*, p. 4629–4634, 2014.

16. **Kim J**, Franco E, Synthetic biochemical devices for programmable dynamic behaviors, Chapter 12 in *A Systems Theoretic Approach to Systems and Synthetic Biology II: Analysis and Design of Cellular Systems*, Kulkarni V, Stan G-B, Raman K (eds.), Springer, 2014.
17. Yeung E, **Kim J**, Murray RM, Resource competition as a source of non-minimum phase behavior in transcription-translation systems, *IEEE Conference on Decision and Control*, p. 4060–4067, 2013.
18. Tuza ZA, Singhal V, **Kim J**, Murray RM, An *in silico* modeling toolbox for rapid prototyping of circuits in a biomolecular 'breadboard' system, *IEEE Conference on Decision and Control*, p. 1404–1410, 2013.
19. Franco E, **Kim J**, Simmel FC, Transcription Oscillators, Chapter 4 in *Multiscale Analysis and Nonlinear Dynamics: From Genes to the Brain*, Misha (Meyer) Z. Pesenson (ed.), Wiley-VCH Verlag GmbH & Co. KGaA, 2013.
20. Yeung E*, **Kim J***, Yuan Y, Gonçalves J, Murray RM, Quantifying crosstalk in biochemical systems, *IEEE Conference on Decision and Control*, p. 5528–5535, 2012. *, co-corresponding authors.
21. Kulkarni VV, Chanyaswady T, Riedel M, **Kim J**, Robust tunable *in vitro* transcriptional oscillator networks, *50th Annual Allerton Conference on Communication, Control, and Computing*, p. 114–119, 2012.
22. **Kim J**, Murray RM, Analysis and design of a synthetic transcriptional network for exact adaptation, *IEEE Biomedical Circuits and Systems Conference*, p. 345–348, 2011.
23. **Kim J**, Synthetic Networks, Chapter 10 in *Automation in proteomics and genomics: an engineering case-based approach*, Alterovitz G, Benson R, Ramoni M (eds.), John Wiley & Sons, 2009.
24. **Kim J**, Hopfield JJ, Winfree E, Neural network computation by *in vitro* transcriptional circuits, *Advances in Neural Information Processing Systems* 17:681–688, 2004.